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#9/52 SW 1633
2/4-02 PCT

ENTERED

RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: US/09/700,354A   TIME: 16:13:36

Input Set : A:\SeqList for IRVN-007CIP2.txt
Output Set: C:\CRF3\05292001\I700354A.raw

SEQUENCE LISTING
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 5 (1) GENERAL INFORMATION:
 7       (i) APPLICANT: Gatanaga, Tetsuya
 8                      Granger, Gale A.
10      (ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
11                               Factor Receptor Releasing Enzyme Activity.
13     (iii) NUMBER OF SEQUENCES: 154
15      (iv) CORRESPONDENCE ADDRESS:
16           (A) ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP
17           (B) STREET: 200 MIDDLEFIELD ROAD, #200
18           (C) CITY: Menlo Park
19           (D) STATE: CA
20           (E) COUNTRY: USA
21           (F) ZIP: 94025
23       (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: Diskette
25           (B) COMPUTER: IBM Compatible
26           (C) OPERATING SYSTEM: Windows
27           (D) SOFTWARE: FastSEQ for Windows Version 2.0b
29      (vi) CURRENT APPLICATION DATA:
C--> 30           (A) APPLICATION NUMBER: US/09/700,354A
C--> 31           (B) FILING DATE: 17-Apr-2001
32           (C) CLASSIFICATION:
34     (vii) PRIOR APPLICATION DATA:
35           (A) APPLICATION NUMBER: 09/081,385
36           (B) FILING DATE: 14-MAY-1998
38           (A) APPLICATION NUMBER: PCT/US99/10793
39           (B) FILING DATE: 14-MAY-1999
42    (viii) ATTORNEY/AGENT INFORMATION:
43           (A) NAME: Francis, Carol L.
44           (B) REGISTRATION NUMBER: 36,513
45           (C) REFERENCE/DOCKET NUMBER: IRVN-007CIP2
47      (ix) TELECOMMUNICATION INFORMATION:
48           (A) TELEPHONE: 650-327-3400
49           (B) TELEFAX: 650-327-3231
50           (C) TELEX:
53 (2) INFORMATION FOR SEQ ID NO: 1:
55       (i) SEQUENCE CHARACTERISTICS:
56           (A) LENGTH: 4047 base pairs
57           (B) TYPE: nucleic acid
58           (C) STRANDEDNESS: double
59           (D) TOPOLOGY: linear
61      (ii) MOLECULE TYPE: Genomic DNA
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
65 AAGCTTTTTG CTTTCCTTCC CCGGGAAAGG CCGGGGCCAG AGACCCGCAC TCGGACCAGG      60
66 CGGGGGCTGC GGGGCCAGAG TGGGCTGGGG AGGGCTGGGA GGGCGTCTGG GGCCGGCTCC     120
67 TCCAGGCTGG GGGCCGCCAG CTCCGGGAAG GCAGTCCTGG CCTGCGGATG GGGCCGCGCG     180
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 68   TGGGGCCCGG CGGGGCGGCC TCGGGAGGCG TCCAGGCTGC GGGAGCGGGA GGAGCGGCCG    240
 69   TGCGGGCGCC AGCGCCGTGG GTGGAGGTCG CCGTCCCTCC TGAGGGGCAG CCAGTGCGTT    300
 70   TGGGACCCGG GAGCAGAGCC CGCGCCTCCC CAGCGGCCTC CCCGGGGGTC TCACCGGGTC    360
 71   ACCCGAGAGC GGAGGCCCCG GCTCCGCAGA AACCCGGGGC GGCCGCGGGG AAGCAGCGCC    420
 72   CTCAGGCGTC GGAGGAGCCC CCAGAAGGAC CTCGCGCCTT CCCGCCGGGC TCCGACCGCC    480
 73   TGGGTTCGGT GCGGGACGGC CCAGGCCGCC AGGACCCCCA AGCGCAGCTC AGTCTGCGGG    540
 74   GCACGACCCA GAGGCCAGCA GCAGAGGACG GGGCCGGGGC CGGGAGAGGG CGGGGAGGGC    600
 75   GCTCCTGGGA GGTCAAGGCC AGGGCTAGAC TTTCAGGGTC ATGGCCTGGC CCCTCATCCC    660
 76   CAGGGAGGTG AGGGGGCTCT GTGAGCAGAG GGGGCCCCGG TGGAGAAGGC GCTGCTAGCC    720
 77   AGGGGCGGGG CAGGAGCCCA GGTGGGGACT TAAGGGTGGC TGAAGGGACC CTCAGGCTGC    780
 78   AGGGATAGGG AGGGAAGCTA GGGGTGTGGC TTGGGGAGGT GCTGGGGGAC CGCGGGCGCC    840
 79   CTTTATTCTG AAGCCGAATG TGCTGCCGGA GTCCCCAGTG ACCTAGAAAT CCATTTCAAG    900
 80   ATTTTCAGGA GTTTCAGGTG GAGACAAAGG CCAGGCCCAG GTGAAAATGT GGCAGTGACA    960
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 82   CGGGGACCAG AATTTTTTAA AACGCATCTG AGATGCGTTT GGCAGACTCA TAGTTGTTTT   1080
 83   CCTTTCACGG AGAAAGTGTG GGCAGAAGCC AGCTCTAAAG CCCAGGCTGC CCAGCCTGCA   1140
 84   CTGGCAGAGC TGACGGAAGG CCAGGGCAGA GCCTTCCCTC CCTGTCACAG ACATGAGCCC   1200
 85   TGGAGATCTG GAATGAGGCA GATGTGCCCA GGGAAAGCTG ATCCGCCCCG ACCCAGGGCC   1260
 86   CCCCGGGTGC CCCTTTGAGC GTGGAATCGT TGCCAGGTCA TGGCTCCCTG CTATCGAACA   1320
 87   CCGGACACGG GTCGTGTGCT GCACCTGGCA GTTGCAGGAC CGACACCCAC AATGCCTTAA   1380
 88   GAGGTGATGA CTGCCTTCCA GGGGCCTGGC TGGCTGACAC TTTGCATGGC TCCTGGAGAA   1440
 89   GAGGGATTGA GTGGAGTCCA CGGGTCATGG CCACGTCCTG GGTGCTGCCT CTGAGGCAGG   1500
 90   GCCCGGCTGG GGTGAGAAGG GGCTGGAGAC AGGTTCCTGC CAGTTCAGCC TCTAACCGGT   1560
 91   GGTCTTCATG CCTAGGAACC CACTGGGGGC TTATGAAACT GCAGGTGGCT GAGTCCTTGC   1620
 92   CATGGGGTCT CTCCTTCAGG AGGTCTGGGT GGGGCCGGAG ACTGTACCCC ACAAAGGGTC   1680
 93   CCAGGTGAGG CGGATGTGGC CTGGCGCTGT GTGGCTCTGG ACCTAGTCCT TGGGCTTGGG   1740
 94   CTGGCGCCCA GGGCCTGGGC TTGAGACAGC TGTGACGCAG GCAAGCCATT TACCCCGTTT   1800
 95   GTGGGGACAT TACATCTTCC TAGCTTGGAA CACACAGGCA GCCAGGGTTG TTATCCACAT   1860
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 98   TTACAATTCC AGGGACAAGA GCGATGCATG TGAGGTGTGG CAAATCTCAC TGTTCAACTG   2040
 99   GAGAAATCAG AGACAGCTTC CTGGAGGCAG TGACACCTGG ACAGGCTTCT CCACAGGAGG   2100
100   AAGCGAGTGA GAGAAGCCAA CTGGGATGGA CCCATCATGT AGGGGGAACA GTGCGCGCAG   2160
101   AACCAACAAC CACCCCCACC CTAGGCCCAG AGCTCACGGA GAGAGCTGGG CCTCTCGGGG   2220
102   TGACTACATA GTTCCCTGCT GGATCTTAGG TCTTGTCCTT GGGCAGCTCT GCTGAGACCT   2280
103   CTATGCCTGT TCCAGGCTGC ACCAAGGTTT TGTGACTATT GGTCTGGGGT TGTTTTGCAG   2340
104   CAACTGAAGT GTTCTGTTGT AAAACAGGCA CTTGATTTGC TGGAAGGAAT GCTGTTTGTT   2400
105   CTTGCTGCGA CAAACATTGA GCAGCATTTA GTGGGCGGTT TATATCTTGT GGAGTAATGG   2460
106   GTGTTTTTGA AGTCTGTCCT GGGTACTGCA CATTAAAAGG AATATCATTT TCTGAAACAT   2520
107   TGCTATTTTC CACACCAGAA ATCATATCCT CTTGCTGGTC CATGTCTGAA GACCTTACAC   2580
108   GAGAAAGTCT TAATGTAAGT TTAGTAGAGT CCTTGGATGG AGAACTAATT ATATCATACA   2640
109   TTGCCGCTTT CTCACTCTGC TCTTTTTCAT CCTTGCCTAA TTTCATTTTC TTCTGCTTCT   2700
110   TTTGTTTTCT TTCTGGAGAA TCTAGCAAGA TATCTGGTGG AACATCTCGA GGTGATGAAC   2760
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112   TTCCAGCAGG GGAGCATACT GGCTGTGGAG ATCTCAAGGG AAAAGATGCA GCATTCCTCA   2880
113   TTGTTGAAGA ATCTCCATCG TCACTACTTA GCCTGTGCAC CATGTGTAGG TAGTCCTCAC   2940
114   TTGAACCATG TCTAGGATTA TCAGCATGAT GATTAGCTGA ATTGCCAGAC AACGGACCAG   3000
115   AAACTTTATT ATCATGTATG TTTCTCAAAC CACCTGCAAC AATGGGACTT GATACCGATG   3060
116   CTTGTTGCAT CTGTGGATGT GTTGTGTAAC TTGAAGGATG GGAATATGGC ATGTATCCTG   3120
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117   CAGGGCTTTG TGGGGCGTAT GGACTAGGCA CTGGGCTATT TTGCTGTGGC ATAAATCTGT    3180
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119   GTTGATAATT GGAAGATGCA GGACTACTGT GCATGGAATT CTGAGAAAGT TTATACTGAG    3300
120   ACATCATCAT TCCACTTTGT ACATATCTGT TCTGCATGCT TTTCTCCCTG AAAACATTAG    3360
121   GACTCCTTGC CAGGACGGCC TGCAACAAGA CTGGTATGTC ACCTTCTGGG TCATCACTGC    3420
122   CAAGGTTATC TTTCAACTCT ATGTGATCTG TTGATACCTG GTTGAGGCTA TGGACAAGCT    3480
123   GTGAAACCAA ATTGTCATCC CTACAAGCCA AAAGGCAGTT CACCTCTTCT GCTATTCGTG    3540
124   CATTAAAGAG AAGGCTCTTT GTAGTTGTAG CAGGTAAAGG AGATGGAAGA GGCAGCTGGT    3600
125   TCAGGAGGTC TGTGAGACTA GCAATCCCCG CAAGAGTAGT AATGGGGACA TGGGGCATAT    3660
126   CCCCATTCAT CCTGAATTTC TGGAATGGTG TTGCCTATAA AAGTACTTAG TTCAGGTGCC    3720
127   AGCTGTCATT ACTTCCCATT TCCCAAACAC TGGGCGAATC GGCGTCTGAA TCCAAGGGGA    3780
128   GGCCGAGGCC GCTGTGGCGA GAGACTATAA TCCGGGCCGG GAGGGGGGGC GGCTACGGCT    3840
129   CCTCTTCCGT CTCCTCAGTG CGGGGAACAT GTAGAGCCGG GGGGAGACCA GCCGAGAAGA    3900
130   CAAATCGTTG CTTCTTCTTC CTCCTCCTCC TCCTTCTCCC ACATAGAAAC ACTCACAAAC    3960
131   ACCCGACCAC GGGCCCGAGC TACCGGGGGG GCATCGCCGC GGGCCCGGGA ACCAATTCTC    4020
132   CTGTCGGCGG GGGCGTCCTT TGGATCC                                        4047
134   (2) INFORMATION FOR SEQ ID NO: 2:
136       (i) SEQUENCE CHARACTERISTICS:
137           (A) LENGTH: 739 base pairs
138           (B) TYPE: nucleic acid
139           (C) STRANDEDNESS: double
140           (D) TOPOLOGY: linear
142       (ii) MOLECULE TYPE: Genomic DNA
144       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
146   GGATCCAAAG GTCAAACTCC CCACCTGGCA CTGTCCCCGG AGCGGGTCGC GCCCGGCCGG      60
147   CGCGCGGCCG GGCGCTTGGC GCCAGAAGCG AGAGCCCCTC GGGGCTCGCC CCCCCGCCTC     120
148   ACCGGGTCAG TGAAAAAACG ATCAGAGTAG TGGTATTTCA CCGGCGGCCC GCAGGGCCGG     180
149   CGGACCCCGC CCCGGGCCCC TCGCGGGGAC ACCGGGGGGG CGCCGGGGGC CTCCCACTTA     240
150   TTCTACACCT CTCATGTCTC TTCACCGTGC CAGACTAGAG TCAAGCTCAA CAGGGTCTTC     300
151   TTTCCCCGCT GATTCCGCCA AGCCCGTTCC CTTGGCTGTG GTTTCGCTGG ATAGTAGGTA     360
152   GGGACAGTGG GAATCTCGTT CATCCATTCA TGCGCGTCAC TAATTAGATG ACGAGGCATT     420
153   TGGCTACCTT AAGAGAGTCA TAGTTACTCC CGCCGTTTAC CCGCGCTTCA TTGAATTTCT     480
154   TCACTTTGAC ATTCAGAGCA CTGGGCAGAA ATCACATCGC GTCAACACCC GCCGCGGGCC     540
155   TTCGCGATGC TTTGTTTTAA TTAAACAGTC GGATTCCCCT GGTCCGCACC AGTTCTAAGT     600
156   CGGCTGCTAG GCGCCGGCCG AAGCGAGGCG CCGCGCGGAA CCGCGGCCCC CGGGGCGGAC     660
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158   CCGAAGAAGA AGGGGGAAA                                                  739
160   (2) INFORMATION FOR SEQ ID NO: 3:
162       (i) SEQUENCE CHARACTERISTICS:
163           (A) LENGTH: 233 base pairs
164           (B) TYPE: nucleic acid
165           (C) STRANDEDNESS: double
166           (D) TOPOLOGY: linear
168       (ii) MOLECULE TYPE: Genomic DNA
170       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
172   CAAGAGTGGC GGCCGCAGCA GGCCCCCCGG GTGCCCGGGC CCCCCTCGAG GGGGACAGTG      60
173   CCCCCGCCGC GGGGGCCCCG CGGCGGGCCG CCGCCGGCCC CTGCCGCCCC GACCCTTCTC     120
174   CCCCCGCCGC CGCCCCCACG CGGCGCTCCC CCGGGGAGGG GGGAGGACGG GGAGCGGGGG     180
175   AGAGAGAGAG AGAGAGAGGG CGCGGGGTGG CTCGTGCCGA ATTCAAAAAG CTT            233
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177 (2)  INFORMATION FOR SEQ ID NO: 4:
179       (i)  SEQUENCE CHARACTERISTICS:
180             (A)  LENGTH: 2998 base pairs
181             (B)  TYPE: nucleic acid
182             (C)  STRANDEDNESS: double
183             (D)  TOPOLOGY: linear
185       (ii)  MOLECULE TYPE: Genomic DNA
187       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
189  GGATCCAAAG AATTCGGCAC GAGGTAGTCA CGGCTCTTGT CATTGTTGTA CTTGACGTTG      60
190  AGGCTGGTGA GCTTGGAAAA GTCGATGCGC AGCGTGCAGC AGGCGTTGTA GATGTTCTGC     120
191  CCGTCCAGCG ACAGCTTGGC GTGCTGGGCG CTCACGGGGT CCGCATACTG CAGCAGGGCC     180
192  TGGAACTGGT TGTTCTTGGT GAAGGTGATG ATCTTCAACA CTGTGCCGAA CTTGGAGAAA     240
193  ATCTGGTGCA GCACATCCAG GGTCACAGGG TAGAAGAGGT TCTCCACGAT GATCCTGAGC     300
194  ACGGGGCTCT GCCCGGCCAT CGCCATCCCT GCATCCACGG CCGCCGCCGA GGCAGCCAAG     360
195  GCCAGGTTCC CCGACTGGAC CGAGTTCACC GCCTGCAGGG CCGCCTGGGC CCGCGCCTGG     420
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197  CCGCGCAGCA CAGGGGTCAC CGAGGTGTAG TAGTTCACCA TGGTATTGGC AGCCTCCTCC     540
198  GTGTTCATCT CGATGAAGGC CTGGTTTTTC CCCTTCAGCA TCAGGAGGTT GGTGACCTTC     600
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204  GCTAGAGCTG CAGATTGAGT TGCTGCGTGA GACGAAGCGC AAGTATGAGA GTGTCCTGCA     960
205  GCTGGGCCGG GCACTGACAG CCCACCTCTA CAGCCTGCTG CAGACCCAGC ATGCACTGGG    1020
206  TGATGCCTTT GCTGACCTCA GCCAGAAGTC CCCAGAGCTT CAGGAGGAAT TTGGCTACAA    1080
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208  CTTTGTCTCT AGCATCAACA CATTGGTCAC CAAGACCATG AAGACACGC TCATGACTGT    1200
209  GAAACAGTAT GAGGCTGCCA GGCTGGAATA TGATGCCTAC CGAACAGACT TAGAGGAGCT    1260
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211  CCAGGCCCAT CGGGACAAGT ATGAGAAGCT GCGGGGAGAT GTGGCCATCA AGCTCAAGTT    1380
212  CCTGGAAGAA AACAAGATCA AGGTGATGCA CAAGCAGCTG CTGCTCTTCC ACAATGCTGT    1440
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214  CAAGCTGCGG CCTCCAGGAG CTGAGAAACC CTCCTGGCTA GAGGAGCAGT GAGCTGCTCC    1560
215  CAGCCCAACT TGGCTATCAA GAAAGACATT GGGAAGGGCA GCCCCAGGGT GTGGGAGATT    1620
216  GGACATGGTA CATCCTTTGT CACTTGCCCT CTGGCTTGGG CTCCTTTTTC TGGCTGGGGC    1680
217  CTGACACCAG TTTTGCCCAC ATTGCTATGG TGGGAAGAGG GCCTGGAGGC CCAGAAGTTG    1740
218  CTGCCCTGTC TATCTTCCTG GCCACAGGGC TTCATTCCCA GATCTTTTCC TTCCACTTCA    1800
219  CAGCCAACGG CTATGACAAA ACCACTCCCT GGCCAATGGC ATCACTCTTC AGGCTGGGGT    1860
220  GTGCTCCCTG ACCAATGACA GAGCCTGAAA ATGCCCTGTC AGCCAATGGC AGCTCTTCTC    1920
221  GGACTCCCCT GGGCCAATGA TGTTGCGTCT AATACCCTTT GTCTCTCCTC TATGCGTGCC    1980
222  CATTGCAGAG AAGGGGACTG GGACCAAAGG GGTGGGGATA ATGGGAGCC CCATTGCTGG    2040
223  CCTTGCATCT GAATAGGCCT ACCCTCACCA TTTATTCACT AATACATTTT ATTTGTGTTC    2100
224  TCTAATTTAA AATTACCTTT TCATCTTGCT TGATTTTCCT TCAGCTAAAT TAGAAATTTG    2160
225  TAGTTTTTCC CCTAAAAAAT TCAATGGCAT TCTTTCTTAT AAATTACATT CTCTGATTTT    2220
226  CTTGTCAGCC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTTGCTCGCA GTTTGCTCCA    2280
227  TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAT TGAGCTGATC CTTCTGGAGA    2340
228  AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCACA CATCCTGAAC    2400
229  TCCCCAGTCT GGTGTGAGGG GAGGACAGCT GATAACTGGA TATGCAGTGT TCCCAGACAT    2460
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233   AAGATCAGAA GTAGAGCCCA TCAACACTAC AACCCTGCAC TGACTTTCTG ATTTCAAAAG   2700
234   CAACTCTACT CTCTCTGCAA CCCACTCAAA GTTTTTCTTT ACCATTTGGA GCCCTTCAGG   2760
235   AGTTACTTCT TTGAGGTCCC GATAAGACTG TTTGTCTTTC TGTTGGCTTC GATCTCCTGA   2820
236   TGGCCAGAGT CTCCAGGAAT CATTGTCAAT AACATCAGCA AGAACAATTT CTTTGGTGGT   2880
237   TACATCAACA CCAAATTCAA TCTTCATATC AACCAGTGTA CAATTCTGGG GCAACCAGGA   2940
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240   (2) INFORMATION FOR SEQ ID NO: 5:
242       (i) SEQUENCE CHARACTERISTICS:
243           (A) LENGTH: 4152 base pairs
244           (B) TYPE: nucleic acid
245           (C) STRANDEDNESS: double
246           (D) TOPOLOGY: linear
248      (ii) MOLECULE TYPE: Genomic DNA
250      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
252   AAGCTTTTTG TGAAAACCCT AGGATATGTC CCCTCCCTCA CCACACCCAA CCCCCCGCCC     60
253   CTGCCCCAGG ACATGACGAT GCCTCACACA CACACACACA CACACATACA CACAAGGCCG    120
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256   CGGAGGAGGG GCCGGGGCTG CAGGACCTCA GGACTGCAAG GGCAGGAAGG GAAACAGGAC    300
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258   AGGTGGGGCG ATCATAAGAG AAGCAGGGAC GATGGTCCAG CTGAGGGAGC CCTGCAGAGG    420
259   GGGAAAAGCT TCCCATGGAC AGGAGAGAGA AGGGAAGGGG AGAGGAGAGG GTTTCCTTCA    480
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263   GAGGGATGGG GGGCCGGGGG AGGGGCAGGG CGGACTCCAG AGGGCCCGCT GGGGTTTTGA    720
264   AATGAAAGGA GGACTGGTTC TGAAGCCTCT CTCCCTCTTG GTCTCTGTGT TCCCAGAAAG    780
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270   CGCCGGCCCC TGAGACGCGG CGGTGAAGGG AATGGATGCG CACCAGGCCC AGGACGACCA   1140
271   TGAGCACCAG GAAGCCCACG CACACCACAA TGATGAGGGT TGCGGCGCTG GGTATCATGG   1200
272   AGTTTCTGTG GGAGCTGGCT AGGCTGTGTC CAGCCATCTC AGGCGGGGGC TGGTGACCAC   1260
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279   CAATCTCATC CGACATGCGT GTGTCTGTCA CTGTGCCCTG CCAACTCTCA TCCTTTTTGG   1680
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283   ACTCTTCGCT GAAGCACTTG ACAGCAGTGG TGAGGCGCAG GGGCCTGACG CCGGGCGTGG   1920
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:3225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154